

## Evaluation of Performance of the Bio-Crystallography Beamline by Means of Refinement of High-Resolution Crystal Structure

Masahiro Fujihashi<sup>1</sup>(0003200), Takaaki Fukami<sup>1</sup>(0003197), Yoshiki Higuchi<sup>1</sup>(0003193), Akiko Kita<sup>1</sup>(0003194), Kengo Kitadokoro<sup>2</sup>(0003205), Ken Kitano<sup>1</sup>(0003198), Hirofumi Komori<sup>1</sup>(0003201), Terukazu Nogi<sup>1</sup>(0003199), Diane H. Peapus<sup>1</sup>(0003195), Jun-ichi Saito<sup>1</sup>(0003196), Kumiko Sobajima<sup>1</sup>(0003202) and Kunio Miki<sup>1</sup>(0003192)※

<sup>1</sup>Department of Chemistry, Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan and <sup>2</sup>Research Center for Instrumental Analysis, Faculty of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan

The purpose of this project is to evaluate of the Bio-Crystallography Beamline (BL41XU) on the basis of the diffraction data of several proteins which have so far been investigated by using the beamlines of Photon Factory. The comparison of data sets of these protein crystals collected at the beamlines in both SPring-8 and Photon Factory enable us to evaluate the performance of the beamline. The following protein samples were employed for this beamtime; 1) chaperonin 60 from *Paracoccus denitrificans*, 2) photolyase from *Anacystis nidulans*, 3) AhpC protein from *Amphibacillus xylanus*, 4) photosynthetic reaction center from *Chromatium tepidum*, 5) aldehyde reductase from *Sporobolomyces salmonicolor*, 6) chitosanase from *Bacillus circulans*. The diffraction patterns from these protein crystals are very clear and sharp, and probably better qualitatively than those obtained at the Photon Factory. The most remarkable example to show the performance of this beamline may be photosynthetic reaction center from *Chromatium tepidum*.

The reaction centers from purple photosynthetic bacteria are integral membrane proteins that accept energy from light-harvesting pigment protein complexes and start the conversion reaction from light to chemical energy. The reaction center from a thermophilic purple bacterium, *Chromatium tepidum* shows a thermal stability up to 47°C in detergent solutions. Crystals of this reaction center belong to the orthorhombic space group  $P2_12_12_1$ , with  $a=134$  Å,  $b=201$  Å and  $c=85$  Å. The X-ray diffraction pattern

obtained from a crystal with dimensions of  $0.2 \times 0.3 \times 0.8$  mm at the BL41XU beamline is shown in Figure. Diffractions were recorded up to at least 1.8 Å resolution. The present crystals of the *Chromatium tepidum* reaction center will be able to give the most precise structure with the highest resolution for bacterial reaction centers, in case of the use of the BL41XU beamline.



**Figure.** X-ray diffraction pattern of the reaction center from *Chromatium tepidum* at the BL41XU beamline.